

## SEQUENCE LISTING

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Zank, Thorsten

<120> METHOD FOR THE PRODUCTION OF POLYUNSATURATED FATTY ACIDS

<130> 12810-00119-US

<150> PCT/EP2004/000771

<151> 2004-01-29

<150> DE 103 08 836.9

<151> 2003-02-27

<160> 57

<170> PatentIn version 3.3

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<223> Acyl-CoA:lysophospholipid acyltransferase

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His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val	
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Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys	
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Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro	
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195 200 205

Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val  
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His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val  
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Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys  
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 aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg 336  
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 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
 165 170 175  
 agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga 576  
 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
 180 185 190  
 gct ctt ttc ctg agg gag caa ctt ttc aaa agt tcg aaa ttg tac tat 624

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr	
195 200 205	
ggt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca	672
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala	
210 215 220	
ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt	720
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys	
225 230 235 240	
atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt	768
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe	
245 250 255	
ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg	816
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly	
260 265 270	
tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag	864
Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys	
275 280 285	
gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act	912
Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr	
290 295 300	
tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg	960
Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp	
305 310 315 320	
agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc	1008
Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile	
325 330 335	
ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt	1056
Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg	
340 345 350	
ggt agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc	1104
Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu	
355 360 365	
tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac	1152
Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr	
370 375 380	
ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca	1200
Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro	
385 390 395 400	
tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc	1248
Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly	
405 410 415	
ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tgc tct	1296
Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser	

420	425	430	
aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga			1344
Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly			
435	440	445	
aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag			1392
Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu			
450	455	460	
cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca			1440
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala			
465	470	475	480
cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac			1488
Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp			
485	490	495	
gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa			1536
Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu			
500	505	510	
gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa			1578
Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser			
515	520	525	

<210> 10  
 <211> 525  
 <212> PRT  
 <213> Physcomitrella patens

<400> 10

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
1 5 10 15

Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
35 40 45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
50 55 60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
65 70 75 80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
85 90 95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val  
 100 105 110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr  
 115 120 125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser  
 130 135 140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala  
 145 150 155 160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
 165 170 175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
 180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr  
 195 200 205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala  
 210 215 220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys  
 225 230 235 240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe  
 245 250 255

Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly  
 260 265 270

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys  
 275 280 285

Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr  
 290 295 300

Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp  
 305 310 315 320



Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile  
 325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg  
 340 345 350

Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu  
 355 360 365

Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr  
 370 375 380

Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro  
 385 390 395 400

Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly  
 405 410 415

Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser  
 420 425 430

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly  
 435 440 445

Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu  
 450 455 460

His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala  
 465 470 475 480

Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp  
 485 490 495

Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu  
 500 505 510

Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
 515 520 525

<210> 11  
 <211> 1192  
 <212> DNA  
 <213> Physcomitrella patens

<220>  
 <221> CDS  
 <222> (58)..(930)  
 <223> Delta-6-elongase

<400> 11  
 ctgcttcgtc tcattcttggg ggtgtgattc gggagtgggt tgagttggtg gagcgca 57  
 atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc tcg 105  
 Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser  
 1 5 10 15  
 cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat 153  
 Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
 20 25 30  
 acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc 201  
 Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
 35 40 45  
 gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg 249  
 Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
 50 55 60  
 tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg 297  
 Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu  
 65 70 75 80  
 ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt 345  
 Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser  
 85 90 95  
 ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac 393  
 Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr  
 100 105 110  
 tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att 441  
 Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile  
 115 120 125  
 ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc 489  
 Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr  
 130 135 140  
 gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac 537  
 Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His  
 145 150 155 160  
 gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat 585  
 Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His  
 165 170 175  
 cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga 633  
 His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly  
 180 185 190

gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga 681  
 Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg  
 195 200 205

agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg 729  
 Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu  
 210 215 220

aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac 777  
 Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr  
 225 230 235 240

tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att 825  
 Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile  
 245 250 255

ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac 873  
 Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr  
 260 265 270

gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa 921  
 Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys  
 275 280 285

act gag tga gctgtatcaa gccatagaaa ctctattatg ttagaacctg 970  
 Thr Glu  
 290

aagttggtgc tttcttatct ccacttatct ttttaagcagc atcagttttg aaatgatgtg 1030

tgggcgtggt ctgcaagtag tcatcaatat aatcggcctg agcacttcag atggattggt 1090

agaacatgag taaaagcggg tattacgggtg tttattttgt accaaatcac cgcacgggtg 1150

aattgaaata tttcagattt gatcaatttc atctgaaaaa aa 1192

<210> 12  
 <211> 290  
 <212> PRT  
 <213> Physcomitrella patens

<400> 12

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser  
 1 5 10 15

Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
 20 25 30

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
 35 40 45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu

50	55	60
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu		
65	70	75 80
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser		
	85	90 95
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr		
	100	105 110
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile		
	115	120 125
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr		
	130	135 140
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His		
145	150	155 160
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His		
	165	170 175
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly		
	180	185 190
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg		
	195	200 205
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu		
	210	215 220
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr		
225	230	235 240
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile		
	245	250 255
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr		
	260	265 270
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys		
	275	280 285

Thr Glu  
290

<210> 13  
<211> 1410  
<212> DNA  
<213> *Phaeodactylum tricornutum*

<220>  
<221> CDS  
<222> (1)..(1410)  
<223> Delta-5-desaturase

<400> 13  
atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta 48  
Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val  
1 5 10 15  
  
gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt 96  
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
20 25 30  
  
ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat 144  
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
35 40 45  
  
gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt 192  
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
50 55 60  
  
ggg ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat 240  
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
65 70 75 80  
  
acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat 288  
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp  
85 90 95  
  
ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa 336  
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys  
100 105 110  
  
cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg 384  
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu  
115 120 125  
  
gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg 432  
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu  
130 135 140  
  
cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc 480  
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala

145	150	155	160	
tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc				528
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala				
165		170	175	
aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc				576
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly				
180		185	190	
ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa				624
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln				
195		200	205	
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat				672
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp				
210		215	220	
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat				720
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp				
225		230	235	240
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg				768
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met				
245		250	255	
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att				816
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile				
260		265	270	
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac				864
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp				
275		280	285	
aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct				912
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala				
290		295	300	
gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc				960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly				
305		310	315	320
ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg				1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val				
325		330	335	
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc				1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe				
340		345	350	
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa				1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu				
355		360	365	
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt				1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly				
370		375	380	

gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa 1200  
 Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
 385 390 395 400

cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc 1248  
 His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
 405 410 415

ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac 1296  
 Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
 420 425 430

tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac 1344  
 Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
 435 440 445

gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc 1392  
 Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
 450 455 460

ttg acc gga cgg gcg taa 1410  
 Leu Thr Gly Arg Ala  
 465

<210> 14  
 <211> 469  
 <212> PRT  
 <213> *Phaeodactylum tricornutum*

<400> 14

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val  
 1 5 10 15

Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
 20 25 30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
 35 40 45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
 50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
 65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp  
 85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys  
 100 105 110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu  
 115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu  
 130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala  
 145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala  
 165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly  
 180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln  
 195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp  
 210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp  
 225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met  
 245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile  
 260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp  
 275 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala  
 290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly  
 305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val



325                                      330                                      335  
 Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe  
    340                                      345                                      350  
  
 Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu  
    355                                      360                                      365  
  
 Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly  
    370                                      375                                      380  
  
 Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
 385                                      390                                      395                                      400  
  
 His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
    405                                      410                                      415  
  
 Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
    420                                      425                                      430  
  
 Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
    435                                      440                                      445  
  
 Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
    450                                      455                                      460  
  
 Leu Thr Gly Arg Ala  
 465

<210> 15  
 <211> 3598  
 <212> DNA  
 <213> artificial sequence

<220>  
 <221> misc\_feature  
 <222> (1)..(3598)

<223> The sequence is a plant promoter-terminator expression cassette in vector pUC19

<400> 15  
 tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacgggtca                      60  
 cagcttgctct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg                      120

ttggcggggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc	180
accatatgcy gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc	240
attcgccatt caggctgcgc aactgttggg aaggcgatc ggtgcgggcc tcttcgctat	300
tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt	360
tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt cggcgcgccg agctcctcga	420
gcaaatttac acattgccac taaacgtcta aacccttgta atttgttttt gttttactat	480
gtgtgttatg tatttgattt gcgataaatt tttatatattg gtactaaatt tataacacct	540
tttatgctaa cgtttgccaa cacttagcaa tttgcaagtt gattaattga ttctaaatta	600
tttttgtctt cttaaatacat atactaatca actggaaatg taaatatttg ctaatatctt	660
tactatagga gaattaaagt gagtgaatat ggtaccacaa ggtttgagga ttttaattgtt	720
gcaatgctgc atggatggca tatacaccaa acattcaata attcttgagg ataataatgg	780
taccacacaa gatttgaggt gcatgaacgt cacgtggaca aaaggtttag taatttttca	840
agacaacaat gttaccacac acaagttttg aggtgcatgc atggatgcc tgtggaaagt	900
ttaaaaatat tttggaaatg atttgcatgg aagccatgtg taaaaccatg acatccactt	960
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<210> 16  
 <211> 3590  
 <212> DNA  
 <213> artificial sequence

<220>  
 <221> misc\_feature  
 <222> (1)..(3590)

<223> The sequence is a plant promoter-terminator expression cassette in vector pUC19

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 ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180  
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 tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360  
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 gtgtgttatg tatttgattt gcgataaatt tttatatattg gtactaaatt tataacacct 540  
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 tttttgtctt ctaaatacat atactaatca actggaaatg taaatatttg ctaatatctc 660  
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<210> 17
<211> 3584
<212> DNA
<213> artificial sequence

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<220>
<221> misc_feature
<222> (1)..(3584)

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<223> The sequence is a plant promoter-terminator expression cassette in vector
pUC19

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gcaaatttac acattgccac taaacgtcta aacccttgta atttgTTTT gttttactat 480
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<210> 18

<211> 4507

<212> DNA

<213> artificial sequence

<220>

<221> misc\_feature

<222> (1)..(4507)

<223> The sequence is a plant promoter-terminator expression cassette in vector pUC19



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Cys	Lys	Lys	His	Gly	Leu	Val	Tyr	Glu	Asp	Val	Ser	Ile	Ala	Thr	Gly	
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Tyr Lys Met Ile His Pro Tyr His Thr Glu Lys His Leu Glu Lys Met	
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Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp His Pro Ala Arg	
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Ala Trp Tyr Pro Tyr Ile	Ala Pro Lys Val Arg	Glu Ile Cys Ala	
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Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
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Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
 35 40 45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
 50 55 60

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu  
 65 70 75 80

Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser  
 85 90 95

Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr  
 100 105 110

Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile  
 115 120 125

Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr  
 130 135 140

Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His  
 145 150 155 160

Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His  
 165 170 175

His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly  
 180 185 190

Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg  
 195 200 205

Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu  
 210 215 220

Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr  
 225 230 235 240

Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile  
 245 250 255

Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr  
 260 265 270

Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys  
 275 280 285

Thr Glu  
 290

<210> 21  
 <211> 525  
 <212> PRT  
 <213> Phaeodactylum tricornutum, Physcomitrella patens

<400> 21

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn  
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Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe  
 20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln  
 35 40 45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala  
 50 55 60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly  
65 70 75 80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg  
85 90 95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val  
100 105 110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr  
115 120 125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser  
130 135 140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala  
145 150 155 160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
165 170 175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr  
195 200 205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala  
210 215 220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys  
225 230 235 240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe  
245 250 255

Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly  
260 265 270

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys  
275 280 285

Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr  
 290 295 300

Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp  
 305 310 315 320

Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile  
 325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg  
 340 345 350

Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu  
 355 360 365

Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr  
 370 375 380

Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro  
 385 390 395 400

Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly  
 405 410 415

Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser  
 420 425 430

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly  
 435 440 445

Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu  
 450 455 460

His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala  
 465 470 475 480

Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp  
 485 490 495

Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu  
 500 505 510

Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
 515 520 525

<210> 22  
 <211> 469  
 <212> PRT  
 <213> Phaeodactylum tricornutum, Physcomitrella patens

<400> 22

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val  
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Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
 20 25 30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
 35 40 45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
 50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
 65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp  
 85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys  
 100 105 110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu  
 115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu  
 130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala  
 145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala  
 165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly  
 180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln  
 195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp  
 210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp  
 225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met  
 245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile  
 260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp  
 275 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala  
 290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly  
 305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val  
 325 330 335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe  
 340 345 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu  
 355 360 365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly  
 370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
                   420                  425                  430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
           435                  440                  445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
       450                  455                  460

Leu Thr Gly Arg Ala  
 465

<210> 23  
 <211> 26  
 <212> DNA  
 <213> artificial sequence

<220>  
 <221> misc\_feature  
 <222> (1)..(26)  
 <223> polylinker sequence

<400> 23  
 gaattcggcg cgccgagctc ctcgag 26

<210> 24  
 <211> 265  
 <212> DNA  
 <213> artificial sequence

<220>  
 <221> misc\_feature  
 <222> (1)..(265)  
 <223> polylinker-terminator-polylinkers sequence

<400> 24  
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 gacgcctatg atcgcatgat atttgctttc aattctgttg tgcacgttgt aaaaaacctg 120  
 agcatgtgta gctcagatcc ttaccgccgg tttcggttca ttctaataaa tatatcaccc 180  
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 aattcgagct cggcgcgcca agctt 265

<210> 25



<211> 257  
 <212> DNA  
 <213> artificial sequence

<220>  
 <221> misc\_feature  
 <222> (1)..(257)  
 <223> polylinker-terminator-polylinkers sequence

<400> 25  
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 tagctcagat ccttaccgcc gggttcgggt catttctaag aatatatcac ccgttactat 180  
 cgtattttta tgaataatat tctccgttca atttactgat tgcccgtcga cgaattcgag 240  
 ctccggcgcgc caagctt 257

<210> 26  
 <211> 5410  
 <212> DNA  
 <213> artificial sequence

<220>  
 <221> misc\_feature  
 <222> (1)..(5410)  
 <223> plant expression vector with one promoter-terminator expression cassette

<400> 26  
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 ggattttgca atactttcat tcatacacac tctaagtt ttacacgatt ataatttctt 180  
 catagccagc ggatccgata tcgggcccgc tagcggttaac cctgctttaa tgagatatgc 240  
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 tgagcatgtg tagctcagat ccttaccgcc gggttcgggt catttctaag aatatatcac 360  
 ccgttactat cgtattttta tgaataatat tctccgttca atttactgat tgcccgtcga 420  
 gcaaatttac acattgccac taaacgtcta aacccttgta atttgttttt gttttactat 480  
 gtgtgttatg tatttgattt gcgataaatt tttatatttg gtactaaatt tataaacacct 540  
 tttatgctaa cgtttgccaa cacttagcaa ttgcaagtt gattaattga ttctaaatta 600  
 tttttgtctt ctaaatacat atactaatca actggaaatg taaatatttg ctaatatctc 660  
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gcaatgctgc atggatggca tatacaccaa acattcaata attcttgagg ataataatgg	780
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<210> 27
<211> 12093
<212> DNA
<213> artificial sequence

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<220>
<221> misc_feature
<222> (1)..(12093)

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<223> plant expression vector with one promoter-terminator expression cassette

<400> 27

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Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe  
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Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu  
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Phe	Pro	Ser	Leu	Pro	Arg	His	Asn	Leu	Ala	Lys	Thr	His	Ala	Leu	Val		
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Glu	Ser	Phe	Cys	Lys	Glu	Trp	Gly	Val	Gln	Tyr	His	Glu	Ala	Asp	Leu		
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Val	Asp	Gly	Thr	Met	Glu	Val	Leu	His	His	Leu	Gly	Ser	Val	Ala	Gly		
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Lys Thr Glu	

290

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Thr Gly Val His Thr Thr Val Tyr Gly Tyr Glu Lys Thr Gln Val Glu	
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Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
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Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu  
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Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys  
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Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg  
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Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu  
 275 280

<210> 37

<211> 477

<212> PRT

<213> *Phaeodactylum tricornutum*, *Physcomitrella patens*, *Caenorhabditis elegans*

<400> 37

Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala

1	5	10	15
Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp	20	25	30
Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His	35	40	45
Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met	50	55	60
Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met	65	70	75
Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu	85	90	95
Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys	100	105	110
Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr	115	120	125
Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val	130	135	140
Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu	145	150	155
Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His	165	170	175
His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe	180	185	190
Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys	195	200	205
His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val	210	215	220
Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp			



225		230		235		240
Ser Val Gln Gln	Ala Gln Ser Tyr Arg	Glu Leu Gln Ala	Asp Gly Lys			
	245		250		255	
Asp Ser Gly Leu	Val Lys Phe Met Ile	Arg Asn Gln Ser	Tyr Phe Tyr			
	260		265		270	
Phe Pro Ile Leu	Leu Leu Ala Arg Leu	Ser Trp Leu Asn	Glu Ser Phe			
	275		280		285	
Lys Cys Ala Phe	Gly Leu Gly Ala	Ala Ser Glu Asn	Ala Ala Leu Glu			
	290		295		300	
Leu Lys Ala Lys	Gly Leu Gln Tyr Pro	Leu Leu Glu Lys	Ala Gly Ile			
305		310		315		320
Leu Leu His Tyr	Ala Trp Met Leu Thr	Val Ser Ser Gly	Phe Gly Arg			
	325		330		335	
Phe Ser Phe Ala	Tyr Thr Ala Phe Tyr	Phe Leu Thr Ala	Thr Ala Ser			
	340		345		350	
Cys Gly Phe Leu	Leu Ala Ile Val Phe	Gly Leu Gly His	Asn Gly Met			
	355		360		365	
Ala Thr Tyr Asn	Ala Asp Ala Arg Pro	Asp Phe Trp Lys	Leu Gln Val			
	370		375		380	
Thr Thr Thr Arg	Asn Val Thr Gly Gly	His Gly Phe Pro	Gln Ala Phe			
385		390		395		400
Val Asp Trp Phe	Cys Gly Gly Leu Gln	Tyr Gln Val Asp	His His Leu			
	405		410		415	
Phe Pro Ser Leu	Pro Arg His Asn Leu	Ala Lys Thr His	Ala Leu Val			
	420		425		430	
Glu Ser Phe Cys	Lys Glu Trp Gly Val	Gln Tyr His Glu	Ala Asp Leu			
	435		440		445	
Val Asp Gly Thr	Met Glu Val Leu His	His Leu Gly Ser	Val Ala Gly			
	450		455		460	

Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
 465 470 475

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<223> synthetic oligonucleotide

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27

<210> 43

<211> 45

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<222> (1)..(45)

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<400> 43

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45

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51

<210> 46

<211> 33

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33

<210> 47

<211> 53

<212> DNA

<213> artificial sequence

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<222> (1)..(53)

<223> synthetic oligonucleotide

<400> 47

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53

<210> 48

<211> 53

<212> DNA

<213> artificial sequence

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<222> (1)..(53)

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<400> 48

cccaagcttg ggcgcgccgag ctccaattcg tcgacggaca atcagtaa at tga

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<210> 49

<211> 47

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<400> 49  
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24

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26

<210> 53  
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<400> 53  
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<210> 54  
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<210> 55  
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<400> 55  
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<210> 56  
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<400> 57

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